GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 07:25:40 ; Search time 727.75 Seconds
(without alignments)
2735.846 Million cell updates/sec

Title: US-09-227-881-1
Perfect score: 5300
Sequence: 1 atctttgttcagtttacctc.....caggcacctctcagcacagc 5300

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36:*
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	5299	100.0	5299	19	V51361	Human TIGR promote
	2	5298.4	100.0	5300	19	V51362	Human TIGR promote
	3	5298.4	100.0	5300	19	V51363	Human TIGR promote
	4	5298.4	100.0	5300	19	V51365	Human TIGR promote
	5	5298.4	100.0	5300	19	V51366	Human TIGR promote
	6	5298.4	100.0	5300	19	V51367	Human TIGR promote
	7	5286	99.7	5304	19	V51364	Human TIGR promote
	8	5275.4	99.5	6169	19	V51368	Human TIGR upstrea
	9	1858	35.1	2800	21	Z37968	Human GLC1A gene e
c	10	176.4	3.3	283	15	Q63862	AP2 sequence obtd.
c	11	175.2	3.3	162450	21	Z86967	Retinoblastoma bin
c	12	174.2	3.3	282	18	T62346	Consensus Alu repe
c	13	173.6	3.3	17327	14	Q44278	Serglycin - proteo
	14	173.2	3.3	49999	20	Z23900	Human LOBO homolog
c	15	172.8	3.3	452	17	T42809	Polymorphic locus
c	16	172.8	3.3	106746	21	A10225	Human PCTA-1 genom
	17	172	3.2	2932	13	Q25388	TXA2 receptor gene
	18	172	3.2	2932	20	Z32161	Human thromboxane
	19	172	3.2	2932	20	Z32162	Human endothelial
c	20	172	3.2	43069	21	Z36335	Genomic sequence o
c	21	171.6	3.2	10380	18	T67164	Human alpha-N-acet
c	22	171.2	3.2	21721	20	X83427	Human lipolysis st
c	23	171.2	3.2	22976	20	X83426	Genomic region con
	24	171	3.2	54548	21	Z45596	DNA sequence of th
	25	170.8	3.2	2617	21	A23452	cDNA encoding huma
	26	170.4	3.2	3234	16	Q92781	Human thymopoietin
c	27	170	3.2	15056	19	V52967	Carcinoembryonic a
c	28	170	3.2	15056	21	Z99933	DNA sequence of co
c	29	169.6	3.2	2426	21	A06689	Human immunogenic
c	30	169	3.2	5543	18	T75284	Nucleotide sequenc
c	31	168.4	3.2	11288	16	Q90512	CEA clone HindIII-
	32	168.2	3.2	3089	21	Z64958	Membrane-bound pro
	33	167.4	3.2	555	20	V90098	EST clone CW1682.
	34	167.4	3.2	41783	21	A35099	Human adenosine re
c	35	167.4	3.2	138169	21	A34791	Human adenosine re
c	36	167.4	3.2	141589	21	A35005	Human adenosine re
c	37	167.4	3.2	141589	21	A35030	Human adenosine re
	38	167.4	3.2	162450	21	Z86967	Retinoblastoma bin
	39	166.8	3.1	7849	16	Q94109	hML genomic DNA.
c	40	166.4	3.1	1601	21	A35191	Human adenosine re
c	41	166.4	3.1	1601	21	Z46814	Interleukin-10 (IL
c	42	166.4	3.1	1618	12	Q10207	pH15C insert conta
c	43	166.4	3.1	1618	14	Q46958	Human cytokine syn
c	44	166.4	3.1	1618	21	Z86905	Human CSIF coding
c	45	166.4	3.1	1645	21	Z58659	Human interleukin-

ALIGNMENTS

RESULT 1
V51361
ID V51361 standard; DNA; 5299 BP.
XX
AC V51361;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human TIGR promoter region DNA.
XX
KW TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.
XX
OS Homo sapiens.
XX
PN WO9832850-A1.
XX
PD 30-JUL-1998.
XX
PF 09-JAN-1998; 98WO-US00468.
XX
PR 26-SEP-1997; 97US-0938669.
PR 28-JAN-1997; 97US-0791154.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX
DR WPI; 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
PS Claim 34; Fig 1; 105pp; English.
XX

CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter region which is used in a method for diagnosing
CC glaucoma in a patient. The method involves the detection of polymorphisms
CC whose presence is predictive of a mutation affecting TIGR response in the
CC patient and can be diagnostic of glaucoma or steroid sensitivity. Base
CC substitutions and base additions upstream of and within TIGR exons can
CC also be used to diagnose glaucoma.
XX
SQ Sequence 5299 BP; 1482 A; 1151 C; 1235 G; 1431 T; 0 other;

Query Match 100.0%; Score 5299; DB 19; Length 5299;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 atctttgttcagtttacctcagggctattatgaaatgaaatgagataaccaatgtgaaag 60
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Qy      61 tcctataaactgtatagcctccattcggatgtatgtctttggcaggatgataaagaatca 120
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Qy     121 ggaagaaggagtatccacgttagccaagtgtccaggctgtgtctgctcttattttagtga 180
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Qy     181 cagatgttgctcctgacagaagctattcttcaggaaacatcacatccaatatggtaaatc 240
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Qy     241 catcaaacaggagctaagaaacaggaatgagatgggcacttgcccaaggaaaaatgccag 300
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Qy     301 gagagcaaataatgatgaaaaataaacttttccctttgtttttaatttcaggaaaaaatg 360
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Db     301 gagagcaaataatgatgaaaaataaacttttccctttgtttttaatttcaggaaaaaatg 360

Qy     361 atgaggaccaaaatcaatgaataaggaaaacagctcagaaaaaagatgtttccaaattgg 420
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Qy     421 taattaagtatttgttccttgggaagagacctccatgtgagcttgatgggaaaatgggaa 480
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Qy     481 aaacgtcaaaagcatgatctgatcagatcccaaagtggattattatttttaaaaaccagat 540
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Qy     781 gacatggttaaaaggcaaccagaacattgtgagccttcaaagcagcagtgcccctcagca 840
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Qy     841 gggaccctgaggcatttgcctttaggaaggccagttttcttaaggaatcttaagaaactc 900
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Qy     901 ttgaaagatcatgaattttaaccattttaagtataaaacaaatatgcgatgcataatcag 960
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Qy    1021 ggataggtcagaaatcattagaaatcactgtgtccccatcctaacttttcagaatgatc 1080
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Qy    1321 acctgagctcactgcaacctctgcctcccaggttcaagcaattctcctgtctcagcctcc 1380
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Qy    1741 caccatgcttttgtggtaagcctccacatcgttactgaaataagagtatacataaactag 1800
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Qy    1801 ttccatttggggccatctgtgtgtgtgtatagggaggagggcataccccagagactcct 1860
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Qy    1861 tgaagcccccggcagaggtttcctctccagctgggggagccctgcaagcacccggggtcc 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1921 tgggtgtcctgagcaacctgccagcccgtgccactggttgttttgttatcactctctagg 1980
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Qy   1981 gacctgttgctttctatttctgtgtgactcgttcattcatccaggcattcattgacaatt 2040
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Qy   2041 tattgagtacttatatctgccagacaccagagacaaaatggtgagcaaagcagtcactgc 2100
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Qy   2101 cctaccttcgtggaggtgacagtttctcatggaagacgtgcagaagaaaattaatagcca 2160
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Qy   2161 gccaacttaaacccagtgctgaaagaaaggaaataaacaccatcttgaagaattgtgcgc 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2221 agcatcccttaacaaggccacctccctagcgcccccctgctgcctccatcgtgcccggagg 2280
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Qy   2281 cccccaagcccgagtcttccaagcctcctcctccatcagtcacagcgctgcagctggcct 2340
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Qy   2341 gcctcgcttcccgtgaatcgtcctggtgcatctgagctggagactccttggctccaggct 2400
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Qy   2401 ccagaaaggaaatggagagggaaactagtctaacggagaatctggaggggacagtgtttc 2460
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Qy   2461 ctcagagggaaaggggcctccacgtccaggagaattccaggaggtggggactgcagggag 2520
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Qy   2521 tggggacgctggggctgagcgggtgctgaaaggcaggaaggtgaaaagggcaaggctgaa 2580
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Qy   2581 gctgcccagatgttcagtgttgttcacggggctgggagttttccgttgcttcctgtgagc 2640
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Qy   2641 ctttttatcttttctctgcttggaggagaagaagtctatttcatgaagggatgcagtttc 2700
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Qy   2701 ataaagtcagctgttaaaattccagggtgtgcatgggttttccttcacgaaggcctttat 2760
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Qy   2761 ttaatgggaatataggaagcgagctcatttcctaggccgttaattcacggaagaagtgac 2820
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Qy   2821 tggagtcttttctttcatgtcttctgggcaactactcagccctgtggtggacttggctta 2880
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Qy   2941 ggttggctgtgcgaccgtgggcaagtgtctctccttccctgggccatagtcttctctgct 3000
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Qy   3001 ataaagacccttgcagctctcgtgttctgtgaacacttccctgtgattctctgtgagggg 3060
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Qy   3301 ggtagcttttgcctggcattcaaaaactgggccagagcaagtggaaaatgccagagattg 3360
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RESULT 2
V51362
ID V51362 standard; DNA; 5300 BP.
XX
AC V51362;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human TIGR promoter mutant TIGRmt1 DNA.
XX
KW TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation 4337
FT /*tag= a
FT /note= "Wild type C is replaced by G"
XX
PN WO9832850-A1.
XX
PD 30-JUL-1998.
XX
PF 09-JAN-1998; 98WO-US00468.
XX
PR 26-SEP-1997; 97US-0938669.
PR 28-JAN-1997; 97US-0791154.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX
DR WPI; 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
PS Disclosure; Fig 2; 105pp; English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter mutant, TIGRmt1, which is used in a method for
CC diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma.
XX
SQ Sequence 5300 BP; 1482 A; 1151 C; 1236 G; 1431 T; 0 other;

Query Match 100.0%; Score 5298.4; DB 19; Length 5300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 atctttgttcagtttacctcagggctattatgaaatgaaatgagataaccaatgtgaaag 60

Qy     61 tcctataaactgtatagcctccattcggatgtatgtctttggcaggatgataaagaatca 120
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Qy    121 ggaagaaggagtatccacgttagccaagtgtccaggctgtgtctgctcttattttagtga 180
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Qy   2881 tgcaagacggtcgaaaaccttggaatcaggagactcggttttctttctggttctgccatt 2940
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Db   2881 tgcaagacggtcgaaaaccttggaatcaggagactcggttttctttctggttctgccatt 2940

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Qy   3001 ataaagacccttgcagctctcgtgttctgtgaacacttccctgtgattctctgtgagggg 3060
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Qy   3061 ggatgttgagaggggaaggaggcagagctggagcagctgagccacaggggaggtggaggg 3120
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Qy   3121 ggacaggaaggcaggcagaagctgggtgctccatcagtcctcactgatcacgtcagactc 3180
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Qy   3181 caggaccgagagccacaatgcttcaggaaagctcaatgaacccaacagccacatttttcct 3240
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Qy   3241 tccctaagcatagacaatggcatttgccaataaccaaaaagaatgcagagactaactggt 3300
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Qy   3301 ggtagcttttgcctggcattcaaaaactgggccagagcaagtggaaaatgccagagattg 3360
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Qy   3361 ttaaacttttcaccctgaccagcaccccacgcagctcagcagtgactgctgacagcacgg 3420
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Qy   3421 agtgacctgcagcgcaggggaggagaagaaaaagagagggatagtgtatgagcaagaaag 3480
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Qy   3481 acagattcattcaagggcagtgggaattgaccacagggattatagtccacgtgatcctgg 3540
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Qy   3601 cctgatttctaatactatatttttcctttacaagctgagtaattctgagcaagtcacaag 3660
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Qy   3661 gtagtaactgaggctgtaagattacttagtttctccttattaggaactctttttctctgt 3720
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Qy   3721 ggagttagcagcacaagggcaatcccgtttctttttaacaggaagaaaacattcctaagag 3780
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Qy   3841 catttcagcgatgtttactatctgattcagaaaatgagactagtacccttggtcagctg 3900
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Qy   4201 ggattattaacctacagtccagaaagcctgtgaatttgaatgaggaaaaaattacatttt 4260
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Qy   4261 tgtttttaccaccttctaactaaatttaacattttattccattgcgaatagagccataaa 4320
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Qy   4321 ctcaaagtggtaataacagtacctgtgattttgtcattaccaatagaaatcacagacatt 4380
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Qy   4621 catgcacacacacagagtaagaactgatttagaggctaacattgacattggtgcctgaga 4680
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Qy   4801 cttgtgttctggctggctgttatttttctctgtccctgctacgtcttaaaggacttgttt 4860
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Qy   5221 gctccccagtatatataaacctctctggagctcgggcatgagccagcaaggccacccatc 5280
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Db   5281 caggcacctctcagcacagc 5300


RESULT   3
V51363
ID   V51363 standard; DNA; 5300 BP.
XX
AC   V51363;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human TIGR promoter mutant TIGRmt2 DNA.
XX
KW   TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW   diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        4950
FT                   /*tag= a
FT                   /note= "Wild-type C is replaced with T"
XX
PN   WO9832850-A1.
XX
PD   30-JUL-1998.
XX
PF   09-JAN-1998;   98WO-US00468.
XX
PR   26-SEP-1997;   97US-0938669.
PR   28-JAN-1997;   97US-0791154.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Chen H,  Chen P,  Nguyen TD,  Polansky JR;
XX
DR   WPI; 1998-427946/36.
XX
PT   Use of TIGR nucleic acid sequences - used for, e.g. developing
PT   products for diagnosis, prognosis and treatment of glaucoma
XX
PS   Disclosure; Fig 2; 105pp; English.
XX
CC   This sequence is a trabecular meshwork induced glucocorticoid response
CC   protein (TIGR) promoter mutant, TIGRmt2, which is used in a method for
CC   diagnosing glaucoma in a patient. The method involves the detection of
CC   polymorphisms whose presence is predictive of a mutation affecting TIGR
CC   response in the patient and can be diagnostic of glaucoma or steroid
CC   sensitivity. Base substitutions and base additions upstream of and within
CC   TIGR exons can also be used to diagnose glaucoma.
XX
SQ   Sequence 5300 BP; 1482 A; 1151 C; 1235 G; 1432 T; 0 other;


  Query Match             100.0%;  Score 5298.4;  DB 19;  Length 5300;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5299;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 atctttgttcagtttacctcagggctattatgaaatgaaatgagataaccaatgtgaaag 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     61 tcctataaactgtatagcctccattcggatgtatgtctttggcaggatgataaagaatca 120
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Qy    121 ggaagaaggagtatccacgttagccaagtgtccaggctgtgtctgctcttattttagtga 180
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Qy    181 cagatgttgctcctgacagaagctattcttcaggaaacatcacatccaatatggtaaatc 240
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Qy    241 catcaaacaggagctaagaaacaggaatgagatgggcacttgcccaaggaaaaatgccag 300
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Qy    301 gagagcaaataatgatgaaaaataaacttttccctttgtttttaatttcaggaaaaaatg 360
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Qy    841 gggaccctgaggcatttgcctttaggaaggccagttttcttaaggaatcttaagaaactc 900
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Db   1621 taatttcagggattcttgggatggggaatggtgccatgagctgcctgcctagtcccagac 1680

Qy   1681 cactggtcctcatcactttcttccctcatcctcattttcaggctaagttaccatttttatt 1740
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Qy   1741 caccatgcttttgtggtaagcctccacatcgttactgaaataagagtatacataaactag 1800
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Qy   1801 ttccatttggggccatctgtgtgtgtgtataggggaggagggcataccccagagactcct 1860
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Qy   1861 tgaagcccccggcagaggtttcctctccagctgggggagccctgcaagcacccggggtcc 1920
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Qy   1921 tgggtgtcctgagcaacctgccagcccgtgccactggttgttttgttatcactctctagg 1980
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Qy   2041 tattgagtacttatatctgccagacaccagagacaaaatggtgagcaaagcagtcactgc 2100
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RESULT 4
V51365
ID V51365 standard; DNA; 5300 BP.
XX
AC V51365;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human TIGR promoter mutant TIGRmt4 DNA.
XX
KW TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation 4256
FT /*tag= a
FT /note= "Wild-type A is replaced by G"
XX
PN WO9832850-A1.
XX
PD 30-JUL-1998.
XX
PF 09-JAN-1998; 98WO-US00468.
XX
PR 26-SEP-1997; 97US-0938669.
PR 28-JAN-1997; 97US-0791154.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX
DR WPI; 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
PS Disclosure; Fig 2; 105pp; English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter mutant, TIGRmt4, which is used in a method for
CC diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma.
XX
SQ Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 other;

Query Match 100.0%; Score 5298.4; DB 19; Length 5300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy   1081 tgtcatagccctcacacacaggcccgatgtgtctgacctacaaccacatctacaacccaa 1140
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Qy   1981 gacctgttgctttctatttctgtgtgactcgttcattcatccaggcattcattgacaatt 2040
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RESULT   5
v51366
ID   V51366 standard; DNA; 5300 BP.
XX
AC   V51366;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human TIGR promoter mutant TIGRmt5 DNA.
XX
KW   TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW   diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        4262
FT                   /*tag= a
FT                   /note= "Wild-type G is replaced with A"
XX
PN   WO9832850-A1.
XX
PD   30-JUL-1998.
XX
PF   09-JAN-1998;   98WO-US00468.
XX
PR   26-SEP-1997;   97US-0938669.
PR   28-JAN-1997;   97US-0791154.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Chen H,  Chen P,  Nguyen TD,  Polansky JR;
XX
DR   WPI; 1998-427946/36.
XX
PT   Use of TIGR nucleic acid sequences - used for, e.g. developing
PT   products for diagnosis, prognosis and treatment of glaucoma
XX
PS   Disclosure; Fig 2; 105pp; English.
XX
CC   This sequence is a trabecular meshwork induced glucocorticoid response
CC   protein (TIGR) promoter mutant, TIGRmt5, which is used in a method for
CC   diagnosing glaucoma in a patient. The method involves the detection of
CC   polymorphisms whose presence is predictive of a mutation affecting TIGR
CC   response in the patient and can be diagnostic of glaucoma or steroid
CC   sensitivity. Base substitutions and base additions upstream of and within
CC   TIGR exons can also be used to diagnose glaucoma.
XX
SQ   Sequence 5300 BP; 1483 A; 1152 C; 1234 G; 1431 T; 0 other;

  Query Match             100.0%;  Score 5298.4;  DB 19;  Length 5300;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5299;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db   4861 ggatctccagttcctagcatagtgcctggcacagtgcaggttctcaatgagtttgcagag 4920

Qy   4921 tgaatggaaatataaactagaaatatatccttgttgaaatcagcacaccagtagtcctgg 4980
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Qy   4981 tgtaagtgtgtgtacgtgtgtgtgtgtgtgtgtgtgtgtgtgtaaaaccaggtggagata 5040
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Qy   5041 taggaactattattggggtatgggtgcataaattgggatgttctttttaaaaagaaactc 5100
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Qy   5101 caaacagacttctggaaggttattttctaagaatcttgctggcagcgtgaaggcaacccc 5160
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Qy   5221 gctccccagtatatataaacctctctggagctcgggcatgagccagcaaggccacccatc 5280
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RESULT   6
V51367
ID   V51367 standard; DNA; 5300 BP.
XX
AC   V51367;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human TIGR promoter variant TIGRsv1 DNA.
XX
KW   TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW   diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        4406
FT                   /*tag= a
FT                   /note= "Wild-type A is replaced by G"
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XX
PN WO9832850-A1.
XX
PD 30-JUL-1998.
XX
PF 09-JAN-1998; 98WO-US00468.
XX
PR 26-SEP-1997; 97US-0938669.
PR 28-JAN-1997; 97US-0791154.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX
DR WPI; 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
PS Disclosure; Fig 2; 105pp; English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter variant, TIGRsv1, which is used in a method for
CC diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma.
XX
SQ Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 other;

Query Match 100.0%; Score 5298.4; DB 19; Length 5300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 atctttgttcagtttacctcagggctattatgaaatgaaatgagataaccaatgtgaaag 60
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Qy     61 tcctataaactgtatagcctccattcggatgtatgtctttggcaggatgataaagaatca 120
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Qy    121 ggaagaaggagtatccacgttagccaagtgtccaggctgtgtctgctcttattttagtga 180
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Qy    181 cagatgttgctcctgacagaagctattcttcaggaaacatcacatccaatatggtaaatc 240
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Qy    241 catcaaacaggagctaagaaacaggaatgagatgggcacttgcccaaggaaaaatgccag 300
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Qy    481 aaacgtcaaaagcatgatctgatcagatcccaaagtggattattatttaaaaaccagat 540
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Qy    781 gacatggttaaaaggcaaccagaacattgtgagccttcaaagcagcagtgcccctcagca 840
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Qy    841 gggaccctgaggcatttgcctttaggaaggccagttttcttaaggaatcttaagaaactc 900
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Qy    901 ttgaaagatcatgaattttaaccattttaagtataaaacaaatatgcgatgcataatcag 960
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Qy   1201 tgtgcagcccatcccgctccacaggaagtctccccactctagacttctgcatcacgatgt 1260
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Qy   1801 ttccatttggggccatctgtgtgtgtgtatagggaggagggcataccccagagactcct 1860
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Qy   3661 gtagtaactgaggctgtaagattacttagtttctccttattaggaactctttttctctgt 3720
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Db   3661 gtagtaactgaggctgtaagattacttagtttctccttattaggaactctttttctctgt 3720
Qy   3721 ggagttagcagcacaagggcaatcccgtttcttttaacaggaagaaaacattcctaagag 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 ggagttagcagcacaagggcaatcccgtttcttttaacaggaagaaaacattcctaagag 3780
Qy   3781 taaagccaaacagattcaagcctaggtcttgctgactatatgattggtttttgaaaaat 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3841 catttcagcgatgtttactatctgattcagaaaatgagactagtacccttttggtcagctg 3900
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Qy   3961 aagaatagaatctttagagcaaactgtgtttctccactctggaggtgagtctgccagggc 4020
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Qy   4021 agtttggaaatatttacttcacaagtattgacactgttgttggtattaacaacataaagt 4080
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Db   4021 agtttggaaatatttacttcacaagtattgacactgttgttggtattaacaacataaagt 4080

Qy   4081 tgctcaaaggcaatcattatttcaagtggcttaaagttacttctgacagttttggtatat 4140
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Qy   4141 ttattggctattgccatttgctttttgttttttctctttgggtttattaatgtaaagcag 4200
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Qy   4201 ggattattaacctacagtccagaaagcctgtgaatttgaatgaggaaaaaattacatttt 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4261 tgtttttaccaccttctaactaaatttaacattttattccattgcgaatagagccataaa 4320
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Qy   4561 atatatttgaaaacatctttctgagaagagttccccagatttcaccaatgaggttcttgg 4620
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Qy   4621 catgcacacacacagagtaagaactgatttagaggctaacattgacattggtgcctgaga 4680
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Qy   4681 tgcaagactgaaattagaaagttctcccaaagatacacagttgttttaaagctaggggtg 4740
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Qy   4801 cttgtgttctggctggctgttatttttctctgtccctgctacgtcttaaaggacttgttt 4860
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Qy   4921 tgaatggaaatataaactagaaatatatccttgttgaaatcagcacaccagtagtcctgg 4980
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Qy   4981 tgtaagtgtgtgtacgtgtgtgtgtgtgtgtgtgtgtgtgtgtaaaaccaggtggagata 5040
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Qy   5041 taggaactattattggggtatgggtgcataaattgggatgttctttttaaaaagaaactc 5100
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Qy   5221 gctccccagtatatataaacctctctggagctcgggcatgagccagcaaggccacccatc 5280
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Db   5281 caggcacctctcagcacagc 5300
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RESULT 7
V51364
ID V51364 standard; DNA; 5304 BP.
XX
AC V51364;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human TIGR promoter mutant TIGRmt3 DNA.
XX
KW TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation 4997..5002
FT /*tag= a
FT /note= "Wild-type TG is replaced with TGTGTG"
XX
PN WO9832850-A1.
XX
PD 30-JUL-1998.
XX
PF 09-JAN-1998; 98WO-US00468.
XX
PR 26-SEP-1997; 97US-0938669.
PR 28-JAN-1997; 97US-0791154.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX
DR WPI; 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
PS Disclosure; Fig 2; 105pp; English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter mutant, TIGRmt3, which is used in a method for
CC diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR

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CC   response in the patient and can be diagnostic of glaucoma or steroid
CC   sensitivity. Base substitutions and base additions upstream of and within
CC   TIGR exons can also be used to diagnose glaucoma.
XX
SQ   Sequence 5304 BP; 1482 A; 1152 C; 1237 G; 1433 T; 0 other;


  Query Match          99.7%;  Score 5286;  DB 19;  Length 5304;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 5300;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    1;

Qy      1 atctttgttcagtttacctcagggctattatgaaatgaaatgagataaccaatgtgaaag 60
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Qy     61 tcctataaactgtatagcctccattcggatgtatgtctttggcaggatgataaagaatca 120
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Qy    121 ggaagaaggagtatccacgttagccaagtgtccaggctgtgtctgctcttattttagtga 180
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Qy    181 cagatgttgctcctgacagaagctattcttcaggaaacatcacatccaatatggtaaatc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    241 catcaaacaggagctaagaaacaggaatgagatgggcacttgcccaaggaaaaatgccag 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 catcaaacaggagctaagaaacaggaatgagatgggcacttgcccaaggaaaaatgccag 300

Qy    301 gagagcaaataatgatgaaaaataaacttttccctttgtttttaatttcaggaaaaaatg 360
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Qy    421 taattaagtatttgttccttgggaagagacctccatgtgagcttgatgggaaaatgggaa 480
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Qy    481 aaacgtcaaaagcatgatctgatcagatcccaaagtggattattatttaaaaaccagat 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 aaacgtcaaaagcatgatctgatcagatcccaaagtggattattatttaaaaaccagat 540

Qy    541 ggcatcactctggggaggcaagttcaggaaggtcatgttagcaaaggacataacaataac 600
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Qy    601 agcaaaatcaaaattccgcaaatgcaggaggaaaatggggactgggaaagctttcataac 660
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Qy    661 agtgattaggcagttgaccatgttcgcaacacctccccgtctataccagggaacacaaaa 720
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Qy    721 attgactgggctaagcctggactttcaagggaaatatgaaaaactgagagcaaaacaaaa 780
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Qy    781 gacatggttaaaaggcaaccagaacattgtgagccttcaaagcagcagtgcccctcagca 840
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Qy    841 gggaccctgaggcatttgcctttaggaaggccagttttcttaaggaatcttaagaaactc 900
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Qy    901 ttgaaagatcatgaattttaaccattttaagtataaaacaaatatgcgatgcataatcag 960
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1741 caccatgcttttgtggtaagcctccacatcgttactgaaataagagtatacataaactag 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1801 ttccatttggggccatctgtgtgtgtgtatagggaggagggcataccccagagactcct 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2401 ccagaaaggaaatggagagggaaactagtctaacggagaatctggaggggacagtgtttc 2460
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Qy   2461 ctcagagggaaaggggcctccacgtccaggagaattccaggaggtggggactgcagggag 2520
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Qy   2701 ataaagtcagctgttaaaattccagggtgtgcatgggttttccttcacgaaggcctttat 2760
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RESULT 8
V51368
ID V51368 standard; DNA; 6169 BP.
XX
AC V51368;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human TIGR upstream region and exon 1 DNA.
XX
KW TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
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FT		/number= 1
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FT		/*tag= b
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FT		/note= "partial coding sequence"
FT	intron	5941..6169
FT		/*tag= c
FT		/number= 1
FT		/note= "partial intron sequence"

XX
PN WO9832850-A1.
XX
PD 30-JUL-1998.
XX
PF 09-JAN-1998; 98WO-US00468.
XX
PR 26-SEP-1997; 97US-0938669.
PR 28-JAN-1997; 97US-0791154.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX
DR WPI; 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
PS Claim 37; Fig 3; 105pp; English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) upstream region and exon 1. This DNA sequence can be used
CC in a method for diagnosing glaucoma in a patient. The method involves the
CC detection of polymorphisms whose presence is predictive of a mutation
CC affecting TIGR response in the patient and can be diagnostic of glaucoma
CC or steroid sensitivity. Base substitutions and base additions upstream of
CC and within TIGR exons can also be used to diagnose glaucoma.
XX
SQ Sequence 6169 BP; 1702 A; 1389 C; 1491 G; 1587 T; 0 other;

Query Match 99.5%; Score 5275.4; DB 19; Length 6169;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5298; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Db   1201 tgtgcagcccatcccgctccacaggaagtctccccactctagacttctgcatcacgatgt 1260

Qy   1261 tacagccagaagctccgtgagggtgagggtctgtgtcttacacctacctgtatgctctac 1320
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Qy   1321 acctgagctcactgcaacctctgcctcccaggttcaagcaattctcctgtctcagcctcc 1380
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Qy   1381 cgcgtagctgggactacaggcgcacgcccggctaatttttgtattgttagtagagatggg 1440
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Qy   1441 gtttcaccatattagcccggctggtcttgaactcctgacctcaggtgatccacccacctc 1500
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Qy   1501 agcctcctaaagtgctgggattacaggcatgagtcaccgcgcccggccaagggtcagtgt 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1561 ttaataaggaataacttgaatggtttactaaaccaacagggaaacagacaaaagctgtga 1620
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Qy   1621 taatttcagggattcttgggatggggaatggtgccatgagctgcctgcctagtcccagac 1680
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Qy   1681 cactggtcctcatcactttcttccctcatcctcattttcaggctaagttaccatttttatt 1740
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Qy   2101 cctaccttcgtggaggtgacagtttctcatggaagacgtgcagaagaaaattaatagcca 2160
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Qy   4620 gcatgcacacacacagagtaagaactgatttagaggctaacattgacattggtgcctgag 4679
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Qy   4680 atgcaagactgaaattagaaagttctcccaaagatacacagttgttttaaagctaggggt 4739
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Qy   4740 gaggggggaaatctgccgcttctataggaatgctctccctggagcctggtagggtgctgt 4799
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Qy   4800 ccttgtgttctggctggctgttatttttctctgtccctgctacgtcttaaaggacttgtt 4859
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Qy   4860 tggatctccagttcctagcatagtgcctggcacagtgcaggttctcaatgagtttgcaga 4919
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Qy   4920 gtgaatggaaatataaactagaaatatatccttgttgaaatcagcacaccagtagtcctg 4979
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Qy   4980 gtgtaagtgtgtgtacgtgtgtgtgtgtgtgtgtgtgtgtgtaaaaccaggtggagat 5039
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Qy   5160 ccctgtgcacagccccacccagcctcacgtggccacctctgtcttcccccatgaagggct 5219
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Qy   5280 ccaggcacctctcagcacagc 5300
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Db   5280 ccaggcacctctcagcacagc 5300
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RESULT 9
Z37968
ID Z37968 standard; DNA; 2800 BP.
XX
AC Z37968;
XX
DT 07-FEB-2000 (first entry)
XX
DE Human GLC1A gene exon 1 and flanking sequences.
XX
KW Glaucoma; PCR amplification; primary open wide angle glaucoma;
KW GLC1A gene; exon; human; ss.
XX
OS Homo sapiens.
XX
PN WO9951779-A2.
XX
PD 14-OCT-1999.
XX
PF 07-APR-1999; 99WO-US07671.
XX
PR 07-APR-1998; 98US-0056285.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Stone EM, Sheffield VC, Alward WLM, Fingert J;
XX
DR WPI; 2000-022956/02.
XX
PT Determination of a predisposition to glaucoma by analysing mutations in
PT the GLC1A gene -
XX
PS Disclosure; Fig 1A; 137pp; English.
XX
CC The invention relates to a method for the determination of a
CC predisposition to glaucoma. The method comprises amplifying a GLC1A gene
CC with a primer pair selected from the sequences shown in Z37981-Z38008.
CC The primers are used to determine whether a subject has or has the
CC potential to develop primary open wide angle glaucoma. The present
CC sequence represents the human GLC1A gene exon 1 and flanking sequences.
XX
SQ Sequence 2800 BP; 781 A; 588 C; 673 G; 758 T; 0 other;

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  Query Match           35.1%;  Score 1858;  DB 21;  Length 2800;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1869;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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Qy   3671 aggctgtaagattacttagtttctccttattaggaactctttttctctgtggagttagca 3730
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Qy   3731 gcacaagggcaatcccgtttcttttaacaggaagaaaacattcctaagagtaaagccaaa 3790
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Qy   3791 cagattcaagcctaggtcttgctgactatatgattggtttttttgaaaaatcatttcagcg 3850
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Qy   3851 atgtttactatctgattcagaaaatgagactagtacccttttggtcagctgtaaacaaaca 3910
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Db    600 tatttacttcacaagtattgacactgttgttggtattaacaacataaagttgctcaaagg 659

Qy   4091 caatcattatttcaagtggcttaaagttacttctgacagttttggtatatttattggcta 4150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 caatcattatttcaagtggcttaaagttacttctgacagttttggtatatttattggcta 719

Qy   4151 ttgccatttgctttttgttttttctctttgggtttattaatgtaaagcagggattattaa 4210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 ttgccatttgctttttgttttttctctttgggtttattaatgtaaagcagggattattaa 779

Qy   4211 cctacagtccagaaagcctgtgaatttgaatgaggaaaaaattacatttttgtttttacc 4270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 cctacagtccagaaagcctgtgaatttgaatgaggaaaaaattacatttttgtttttacc 839

Qy   4271 accttctaactaaatttaacattttattccattgcgaatagagccataaactcaaagtgg 4330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 accttctaactaaatttaacattttattccattgcgaatagagccataaactcaaagtgg 899

Qy   4331 taataacagtacctgtgattttgtcattaccaatagaaatcacagacattttatactata 4390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 taataacagtacctgtgattttgtcattaccaatagaaatcacagacattttatactata 959

Qy   4391 ttacagttgttgcagatacgttgtaagtgaaatatttatactcaaaactactttgaaatt 4450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 ttacagttgttgcagatacgttgtaagtgaaatatttatactcaaaactactttgaaatt 1019

Qy   4451 agacctcctgctggatcttgtttttaacatattaataaaacatgtttaaaattttgatat 4510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 agacctcctgctggatcttgtttttaacatattaataaaacatgtttaaaattttgatat 1079

Qy   4511 tttgataatcatatttcattatcatttgtttcctttgtaatctatattttatatatttga 4570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 tttgataatcatatttcattatcatttgtttcctttgtaatctatattttatatatttga 1139

Qy   4571 aaacatctttctgagaagagttccccagatttcaccaatgaggttcttggcatgcacaca 4630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 aaacatctttctgagaagagttccccagatttcaccaatgaggttcttggcatgcacaca 1199

Qy   4631 cacagagtaagaactgatttagaggctaacattgacattggtgcctgagatgcaagactg 4690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 cacagagtaagaactgatttagaggctaacattgacattggtgcctgagatgcaagactg 1259

Qy   4691 aaattagaaagttctcccaaagatacacagttgttttaaagctaggggtgaggggggaaa 4750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 aaattagaaagttctcccaaagatacacagttgttttaaagctaggggtgaggggggaaa 1319

Qy   4751 tctgccgcttctataggaatgctctccctggagcctggtagggtgctgtccttgtgttct 4810
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 tctgccgcttctataggaatgctctccctggagcctggtagggtgctgtccttgtgttct 1379

Qy   4811 ggctggctgttatttttctctgtccctgctacgtcttaaaggacttgtttggatctccag 4870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 ggctggctgttatttttctctgtccctgctacgtcttaaaggacttgtttggatctccag 1439

Qy   4871 ttcctagcatagtgcctggcacagtgcaggttctcaatgagtttgcagagtgaatggaaa 4930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440 ttcctagcatagtgcctggcacagtgcaggttctcaatgagtttgcagagtgaatggaaa 1499

Qy   4931 tataaactagaaatatatccttgttgaaatcagcacaccagtagtcctggtgtaagtgtg 4990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 tataaactagaaatatatccttgttgaaatcagcacaccagtagtcctggtgtaagtgtg 1559

Qy   4991 tgtacgtgtgtgtgtgtgtgtgtgtgtgtgtaaaaccaggtggagatataggaactat 5050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 tgtacgtgtgtgtgtgtgtgtgtgtgtgtgtaaaaccaggtggagatataggaactat 1619

Qy   5051 tattggggtatgggtgcataaattgggatgttctttttaaaaagaaactccaaacagact 5110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 tattggggtatgggtgcataaattgggatgttctttttaaaaagaaactccaaacagact 1679

Qy   5111 tctggaaggttattttctaagaatcttgctggcagcgtgaaggcaaccccccctgtgcaca 5170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 tctggaaggttattttctaagaatcttgctggcagcgtgaaggcaaccccccctgtgcaca 1739

Qy   5171 gccccacccagcctcacgtggccacctctgtcttcccccatgaagggctggctccccagt 5230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 gccccacccagcctcacgtggccacctctgtcttcccccatgaagggctggctccccagt 1799

Qy   5231 atatataaacctctctggagctcgggcatgagccagcaaggccacccatccaggcacctc 5290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 atatataaacctctctggagctcgggcatgagccagcaaggccacccatccaggcacctc 1859

Qy   5291 tcagcacagc 5300
          ||||||||||
Db   1860 tcagcacagc 1869
```

RESULT 10
Q63862/c
ID Q63862 standard; cDNA; 283 BP.
XX
AC Q63862;
XX
DT 29-JAN-1995 (first entry)
XX
DE AP2 sequence obtd. by PCR for tumour specific DNA.
XX
KW Arbitrary primers; AP-PCR; amplification; tumour cells; cancer;
KW insertions; deletions; ss.
XX
OS Synthetic.
XX
PN WO9411531-A.
XX
PD 26-MAY-1994.
XX
PF 12-NOV-1993; 93WO-US10904.
XX
PR 13-NOV-1992; 92US-0975737.
XX
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Ionov Y, Malkhosyan S, Mcclelland M, Peinado MA;
PI Perucho M, Welshj;
XX
DR WPI; 1994-183529/22.
XX
PT Identification of tumour cells - by analysing DNA to determine
PT whether insertions or deletions have occurred in reiterated
PT sequences
XX
PS Disclosure; Page 52; 67pp; English.
XX
CC The sequence was obtd. by PCR with arbitrary PCR primers used to
CC detect insertions or deletions in DNA sequences. Such mutations are
CC markers of cancer so such primers can be used in the diagnosis of
CC cancer, esp. colorectal, stomach or pancreatic tumours.
CC See also Q63837-63.
XX
SQ Sequence 283 BP; 63 A; 77 C; 94 G; 49 T; 0 other;

```
  Query Match             3.3%;  Score 176.4;  DB 15;  Length 283;
  Best Local Similarity   80.4%;  Pred. No. 1.4e-31;
  Matches  222;  Conservative    0;  Mismatches   46;  Indels    8;  Gaps    1;

Qy   1281 gggtgagggtctgtgtcttacacctacctgtatgctctacacctgagctcactgcaacct 1340
          | ||   | |||||  |  |  |     || |    |   | ||  ||||||||||||||
Db    276 GAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAACCT 217

Qy   1341 ctgcctcccaggttcaagcaattctcctgtctcagcctcccgcgtagctgggactacagg 1400
          |  |||||| |||||||||  |||||||||  ||||||||||| ||||||||||  ||||||
Db    216 CCACCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGG 157
```

```
Qy   1401 cg--------cacgcccggctaatttttgtattgttagtagagatggggtttcaccatat 1452
          ||        |||||||||||||||||||||||| |||||||||| |||||||||||| |
Db    156 CGCGCGCCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGT 97

Qy   1453 tagcccggctggtcttgaactcctgacctcaggtgatccacccacctcagcctcctaaag 1512
          | ||| |||||||||||||||||||||||||||||||||||||||||||||| |||||| ||||
Db     96 TGGCCAGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCGGCCTCCCAAAG 37

Qy   1513 tgctgggattacaggcatgagtcaccgcgcccggcc 1548
          ||||||||||||||  |||| |||| ||||| |||
Db     36 TGCTGGGATTACAGGTGTGAGCCACCACGCCCAGCC 1


RESULT 11
Z86967/c
ID   Z86967 standard; DNA; 162450 BP.
XX
AC   Z86967;
XX
DT   16-MAY-2000 (first entry)
XX
DE   Retinoblastoma binding protein-7 genomic DNA sequence.
XX
KW   RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
KW   diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
KW   benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
KW   lymphoma; ds.
XX
OS   Homo sapiens.
XX
PN   WO200000607-A1.
XX
PD   06-JAN-2000.
XX
PF   30-JUN-1999;   99WO-IB01242.
XX
PR   30-JUN-1998;   98US-0091315.
PR   10-DEC-1998;   98US-0111909.
XX
PA   (GEST ) GENSET.
XX
PI   Bougueleret L;
XX
DR   WPI; 2000-117170/10.
XX
PT   Novel nucleic acid and polymorphic markers used for diagnosis of
PT   diseases, especially those involving abnormal cell proliferation and
PT   differentiation -
XX
PS   Claim 1; Page 118-163; 223pp; English.
XX
CC   This sequence represents the retinoblastoma binding protein-7 (RBP-7)
CC   genomic sequence of the invention. The RBP-7 coding sequence and
CC   regulatory sequences are useful for the recombinant production of the
CC   protein and for expressing heterologous nucleic acids. Primers and probes
CC   derived from the RBP-7 nucleotide sequence (e.g. Z87035-Z87099) are
CC   useful for DNA amplification and detection methods. RBP-7 biallelic
CC   markers (see Z86993-Z87034) are useful for diagnosis of disease related
CC   to alteration in the regulation or in the coding regions of the RBP-7
CC   gene and for prognosis/diagnosis of an eventual treatment with
CC   therapeutic agents, especially agents acting on pathologies involving
CC   abnormal cell proliferation and/or differentiation, these include
CC   thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers,
CC   including breast cancer, sarcomas and other neoplasms, bladder cancer,
CC   colon cancer, lung cancer, prostate cancer, various leukaemias, and
CC   lymphomas. RBP-7 antibodies are useful as diagnostic agents.
XX
SQ   Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other;

  Query Match             3.3%;  Score 175.2;  DB 21;  Length 162450;
  Best Local Similarity   78.4%;  Pred. No. 4.1e-30;
  Matches  210;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy   1280 agggtgagggtctgtgtcttacacctacctgtatgctctacacctgagctcactgcaacc 1339
          || ||   | |||||  |  |  |     ||      | | | || || ||||| |||||
Db 141925 AGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCGCTGGCAAGATCTCAGTTCACTACAACC 141866

Qy   1340 tctgcctcccaggttcaagcaattctcctgtctcagcctcccgcgtagctgggactacag 1399
          ||  |||||| |||||| |||||||||||||||| |||||||   ||||||||||||||
Db 141865 TCCACCTCCCGGGTTCAGGCAATTCTCCTGTCTCGGCCTCCCCAATAGCTGGGACTACAG 141806

Qy   1400 gcgcacgcccggctaatttttgtattgttagtagagatggggtttcaccatattagcccg 1459
          || ||||||  |||||||||||||||| |||| |||||||||||||||||| |||| | | |
Db 141805 GCACACGCCAAGCTAATTTTTGTATTTTTAGCAGAGATGGGGTTTCACCCTATTGGTCAG 141746

Qy   1460 gctggtcttgaactcctgacctcaggtgatccacccacctcagcctcctaaagtgctggg 1519
          ||||||||  |||||||||||||||| |||||||||  |||| |||||| ||||||||||
Db 141745 GCTGGTCTCAAACTCCTGACCTCAGATGATCCACCTGCCTCGGCCTCCCAAAGTGCTGGG 141686

Qy   1520 attacaggcatgagtcaccgcgcccggc 1547
          ||||||||  |||| ||| | |||| ||
Db 141685 ATTACAGGTGTGAGCCACTGTGCCCAGC 141658


RESULT 12
T62346/c
ID   T62346 standard; DNA; 282 BP.
XX
AC   T62346;
XX
DT   11-JUN-1997 (first entry)
XX
DE   Consensus Alu repeat sequence.
XX
KW   Bubble; interspersed repetitive element; ligation; annealing; primer;
KW   PCR; polymerase chain reaction; amplification; chromosomal aberration;
KW   genetic disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     22..45
FT                   /*tag= a
FT                   /note= "binds primer 47-23 (T62347)"
FT   primer_bind     216..236
FT                   /*tag= b
FT                   /note= "binds either primer Alu-S (T62348) or
FT                          Alu-J (T62349)"
FT   primer_bind     263..282
FT                   /*tag= c
FT                   /note= "binds primer Alu-end (T62350)"
XX
PN   US5597694-A.
XX
PD   28-JAN-1997.
XX
PF   07-OCT-1993;   93US-0133629.
XX
PR   07-OCT-1993;   93US-0133629.
XX
PA   (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI   Housman DE, Munroe DJ;
XX
DR   WPI; 1997-108321/10.
XX
PT   Amplification of nucleic acid having interspersed repetitive element
PT   - using bubble oligo:nucleotide
XX
PS   Disclosure; Column 19-20; 16pp; English.
XX
CC   The invention relates to the amplification of region of DNA containing
CC   interspersed repetitive elements (IRE) such as the Alu repeat sequence
CC   presented here. The method involves ligating a double stranded DNA
CC   structure with a non-complementary region, a 'bubble', in the
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CC   centre (e.g. see T62343-4), to restriction digested fragments of regions
CC   containing IREs.  The ligation results in a double stranded DNA molecule
CC   containing at least one 'bubble' at either end.  After denaturing the
CC   structure, amplification of the IRE-containing region proceeds by PCR
CC   using primers targeted to the IRE sequence (e.g. see T62347-50) and to
CC   the sequence in the 'bubble' region (e.g. see T62345).  The method can
CC   be used to detect the presence or absence of a chromosomal aberration
CC   e.g. in a genetic disorder, in a test organism.
XX
SQ   Sequence 282 BP; 63 A; 75 C; 90 G; 48 T; 6 other;


  Query Match             3.3%;  Score 174.2;  DB 18;  Length 282;
  Best Local Similarity   78.7%;  Pred. No. 4.6e-31;
  Matches  218;  Conservative    4;  Mismatches   47;  Indels    8;  Gaps    1;

Qy   1280 agggtgagggtctgtgtcttacacctacctgtatgctctacacctgagctcactgcaacc 1339
           :| ||   : |||||  |  |  |     || |    |   | |:  ||||||||||:||
Db    277 RGAGTCTYRCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGCGATCWCGGCTCACTGCARCC 218

Qy   1340 tctgcctcccaggttcaagcaattctcctgtctcagcctcccgcgtagctgggactacag 1399
           ||  |||||  |||||||||| |||||||||| |||||||||||| |||||||||| |||||
Db    217 TCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAG 158

Qy   1400 gcg--------cacgcccggctaatttttgtattgttagtagagatggggtttcaccata 1451
           |||        |||||||||||||||||||||| |||||||||| ||||||||||||
Db    157 GCGCGCGCCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATG 98

Qy   1452 ttagcccggctggtcttgaactcctgacctcaggtgatccacccacctcagcctcctaaa 1511
           || ||| |||||||||||||||||||||||||||||||||||||||||| |||||| |||
Db     97 TTGGCCAGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCGGCCTCCCAAA 38

Qy   1512 gtgctgggattacaggcatgagtcaccgcgcccggcc 1548
           ||||||||||||||||  |||| |||| ||||| |||
Db     37 GTGCTGGGATTACAGGTGTGAGCCACCACGCCCAGCC 1


RESULT  13
Q44278/c
ID   Q44278 standard; DNA; 17327 BP.
XX
AC   Q44278;
XX
DT   24-NOV-1993  (first entry)
XX
DE   Serglycin - proteoglycan peptide core.
XX
KW   Haematopoietic cell secretory granule proteoglycan;
KW   positive; negative; transcriptional regulatory element;
KW   enhancer; eukaryotic promoter; constitutive suppressor;
KW   TATA-box; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_signal     373..621
FT                   /*tag=  a
FT                   /note= "5' regulatory region;
FT                         claim 1-3, page 78"
FT   misc_signal     373..433
FT                   /*tag=  b
FT                   /note= "negative transcriptional regulatory element;
FT                         claim 6 and 9-10, page 78-79"
FT   enhancer        514..541
FT                   /*tag=  c
FT                   /note= "enhancer transcriptional regulatory element;
FT                         claim 11 and 14-15, page 79"
FT   promoter        582..602
FT                   /*tag=  d
FT                   /note= "eukaryotic promoter element;
FT                         claim 16 and 19-20, page 80"
FT   CDS             675..16646
FT                   /*tag=  e
FT                   /label= serglycin
FT   exon            622..753
FT                   /*tag=  f
FT                   /number= 1
FT   exon            9597..9744
FT                   /*tag=  g
FT                   /number= 2
FT   exon            16397..17327
FT                   /*tag=  h
FT                   /number= 1
FT   sig_peptide     675..9598
FT                   /*tag=  i
FT                   /note= "interrupted by exon 1"
FT   misc_RNA        16449..16502
FT                   /*tag=  j
FT                   /note= "serine-glycine rich glycosaminoglycan
FT                         attachment region"
FT   polyA_signal    17062..17067
FT                   /*tag=  k
FT   misc_difference 6135
FT                   /*tag=  l
FT                   /note= "base represented as N in the specification"
XX
PN   WO9313119-A.
XX
PD   08-JUL-1993.
XX
PF   23-DEC-1992;   92WO-US11194.
XX
PR   03-JAN-1992;   92US-0816289.
PR   02-JUL-1992;   92US-0906871.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Avraham S,  Stevens RL;
XX
DR   WPI; 1993-227261/28.
DR   P-PSDB; R39393.
XX
PT   Transcription regulatory elements of ser-glycin gene - specific
PT   for haematopoietic cells, also trans-acting transcriptional
PT   binding factors
XX
PS   Disclosure; Fig 4B-J; 112pp; English.
XX
CC   A negative transcription regulatory element (a constitutive
CC   suppressor) between residues -250 and -190 (see tag b) of the 5'
CC   flanking region of the human serglycin gene, a positive
CC   (hematopoietic cell enhancer) regulatory element located between
CC   residues -118 and -81 (see tag c), an equiv. of the TATA-box and
CC   a novel eukaryotic promoter that utilises such equiv. (see tag d)
CC   are identified.  The regulatory elements, vectors and hosts
CC   provided with these elements, are useful in the control of gene
CC   transcription of heterologous genes in eukaryotic cells, esp.
CC   hematopoietic cells.
XX
SQ   Sequence 17327 BP; 4936 A; 3604 C; 3741 G; 5045 T; 1 other;


  Query Match             3.3%;  Score 173.6;  DB 14;  Length 17327;
  Best Local Similarity   77.2%;  Pred. No. 3.7e-30;
  Matches  227;  Conservative    0;  Mismatches   59;  Indels    8;  Gaps    1;

Qy   1321 acctgagctcactgcaacctctgcctcccaggttcaagcaattctcctgtctcagcctcc 1380
           | ||  |||||||||||||||||||||||||||||||||||| |||||||||| ||||||||||
Db   7766 ATCTCGGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCC 7707

Qy   1381 cgcgtagctgggactacaggcgcacgc--------ccggctaatttttgtattgttagta 1432
           || ||||||||||  ||||| || | |        || ||||||||||||||| ||||||
Db   7706 CGAGTAGCTGGGATGACAGGTGCCCACAATCATATCCAGCTAATTTTTGTATTTTTAGTA 7647

Qy   1433 gagatggggtttcaccatattagcccggctggtcttgaactcctgacctcaggtgatcca 1492
           | |||||||||||||||| || ||| ||||||||| ||||||||||||||||||||||||
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Db   7646 GGGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCA 7587

Qy   1493 cccacctcagcctcctaaagtgctgggattacaggcatgagtcaccgcgcccggccaagg 1552
          ||| |||||| |||| ||||||||||||||||||  |||| |||| | ||||||| |
Db   7586 CCCGCCTCAGTCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCACACCCGGCCGAAA 7527

Qy   1553 gtcagtgtttaataaggaataacttgaatggtttactaaaccaacagggaaaca 1606
          ||   | ||    ||   | ||  ||      |    ||||| | |   ||| |
Db   7526 GTACTTTTTATGGAAAAGACAATGTGGCATTGTAGAAAAACCTATACTTAAAAA 7473


RESULT 14
Z23900
ID   Z23900 standard; DNA; 49999 BP.
XX
AC   Z23900;
XX
DT   25-JAN-2000 (first entry)
XX
DE   Human LOBO homologue genomic DNA fragment 2.
XX
KW   LOBO; long bones; bone development; bone extension; skull; osteopathic;
KW   diagnostic; pharmaceutical; gene therapy; transgenic animal; disease;
KW   spondyloepiphysal dysplasia; achondroplasia; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO9950284-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-EP02055.
XX
PR   27-MAR-1998;   98DE-1013799.
XX
PA   (ROSE/) ROSENTHAL A.
XX
PI   Rosenthal A,  Rump A,  Hess J,  Aigner T,  Wirth T;
XX
DR   WPI; 1999-601320/51.
XX
PT   Nucleic acids encoding proteins which influence bone development,
PT   useful for treating and studying bone disorders -
XX
PS   Example 3; Page 244-271; 391pp; German.
XX
CC   This invention describes novel nucleic acids (I; designated LOBO (long
CC   bones)) encoding proteins influencing bone development in mammals. The
CC   proteins of the invention reduce and/or inactivate bone extension (i.e.
CC   development), with exception of the skull and have osteopathic activity.
CC   The nucleic acid molecules, proteins and antibodies can be used in
CC   diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods
CC   and nucleic acid molecules, etc. are useful for production of transgenic
CC   animals, especially a transgenic mouse for the study of diseases
CC   associated with bone development, e.g. spondyloepiphysal dysplasia and
CC   achondroplasia. This sequence encodes a human LOBO protein described
CC   in the method of the invention.
XX
SQ   Sequence 49999 BP; 11432 A; 13017 C; 12505 G; 13045 T; 0 other;


  Query Match             3.3%;  Score 173.2;  DB 20;  Length 49999;
  Best Local Similarity   81.0%;  Pred. No. 7.2e-30;
  Matches  217;  Conservative    0;  Mismatches   43;  Indels    8;  Gaps    1;

Qy   1320 cacctgagctcactgcaacctctgcctcccaggttcaagcaattctcctgtctcagcctc 1379
          || ||  |||||||||||||||| ||||||  ||||||||| ||||||||| |||||||||
Db   3991 catcttggctcactgcaacctccgcctcctgggttcaagcgattctcctgcctcagcctc 4050

Qy   1380 ccgcgtagctgggactacaggcg--------cacgcccggctaatttttgtattgttagt 1431
          ||| |||||||||| |||| | |        ||||||| |||||||||||||| |||||
Db   4051 ccgagtagctgggattacaagtgcccgccaccacgcccagctaatttttgtatttttagt 4110

Qy   1432 agagatggggtttcaccatattagcccggctggtcttgaactcctgacctcaggtgatcc 1491
          ||||||||||||||||||| || ||| ||||| |||||||||||||| ||||||||||
Db   4111 agagatggggtttcaccatgttggccaggctgatcttgaactcctgacttcaggtgatcc 4170

Qy   1492 acccacctcagcctcctaaagtgctgggattacaggcatgagtcaccgcgcccggccaag 1551
          |||  |||  |||||| |||||| |||||||| ||||||||| |||||||||| |||| |
Db   4171 acctgccttggcctcccaaagtgatgggattataggcatgagccaccgcgcccagccagg 4230

Qy   1552 ggtcagtgtttaataaggaataacttga 1579
               ||  ||||  | |  ||  ||| |
Db   4231 aaagagattttataaggctatttcttaa 4258


RESULT 15
T42809/c
ID   T42809 standard; DNA; 452 BP.
XX
AC   T42809;
XX
DT   04-SEP-1997 (first entry)
XX
DE   Polymorphic locus Q560 sequence.
XX
KW   Primer; PCR; polymerase chain reaction; amplification; polymorphism;
KW   genomic locus; gene mapping; paternity; maternity; children;
KW   forensic science; fingerprinting; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    15..23
FT                   /*tag= a
FT                   /note= "sequence contains between 3-9 undefined
FT                          nucleotides in this region"
FT   repeat_region   27..74
FT                   /*tag= b
FT                   /note= "this specification discloses that the repeat unit
FT                          TAAA (bases 27-30; see below) is repeated 7-12
FT                          times; this sequence contains 12 repeats of the
FT                          TAAA sequence"
FT   repeat_unit     27..30
FT                   /*tag= c
FT                   /note= "repeated 7-12 times; this sequence contains 12
FT                          repeats of this sequence"
FT   repeat_unit     77..359
FT                   /*tag= d
FT                   /rpt_type= Alu repeat
FT   misc_feature    424..432
FT                   /*tag= e
FT                   /note= "sequence contains between 3-9 undefined
FT                          nucleotides in this region"
XX
PN   WO9634979-A2.
XX
PD   07-NOV-1996.
XX
PF   01-MAY-1996;   96WO-CA00275.
XX
PR   01-MAY-1995;   95US-0432023.
XX
PA   (REHO-) CENT RECH HOPITAL SAINTE-JUSTINE.
XX
PI   Labuda D,  Melancon SB,  Tang JQ,  Vanasse M;
XX
DR   WPI; 1996-506179/50.
XX
PT   DNA amplification primer pair - used for simultaneous amplification
PT   of multiple highly polymorphic genomic loci, partic. for
PT   fingerprinting
XX
PS   Example 1; Fig 1; 23pp; English.
XX
CC   This is the sequence of the highly polymorphic locus Q560 which is
```

CC amplified by the primer pair R14B264/Q560mak (T42806-7). The primers
CC also simultaneously amplify the loci Q900 (T42808) and Q120 (T42810).
CC The primers can be used for gene mapping, to assess paternity, maternity
CC and identity of children or in forensic science. In particular, they can
CC be used for the DNA fingerprinting identification of genetically related
CC or unrelated individuals.
XX
SQ Sequence 452 BP; 149 A; 92 C; 106 G; 85 T; 20 other;

Query Match 3.3%; Score 172.8; DB 17; Length 452;
Best Local Similarity 86.4%; Pred. No. 1.2e-30;
Matches 204; Conservative 1; Mismatches 23; Indels 8; Gaps 1;

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Qy   1321 acctgagctcactgcaacctctgcctcccaggttcaagcaattctcctgtctcagcctcc 1380
          | || ||||||||||||| ||||||||||||||||||||| ||||||||| ||||||||||
Db    312 ATCTCAGCTCACTGCAAACTCTGCCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCC 253

Qy   1381 cgcgtagctgggactacaggcg--------cacgcccggctaatttttgtattgttagta 1432
          || :|||||||||| |||||| |        || ||||||||||||||||||| ||||||
Db    252 CGARTAGCTGGGATTACAGGTGCCCGCCACCATGCCCGGCTAATTTTTGTATTTTTAGTA 193

Qy   1433 gagatggggtttcaccatattagcccggctggtcttgaactcctgacctcaggtgatcca 1492
          |||| ||||||||||||  || ||| |||||||||  ||||||||||||||||||||||
Db    192 GAGACGGGGTTTCACCACGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGTGATCTG 133

Qy   1493 cccacctcagcctcctaaagtgctgggattacaggcatgagtcaccgcgcccggcc 1548
          ||| |||||||||||| |||||||||||||||||||||||||| |||| |||||||||
Db    132 CCCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCCCGCCCGGCC 77
```

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Job time: 42641 sec